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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2009; month=4; day=14; hr=7; min=51; sec=51; ms=455;]

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Application No: 10552298 Version No: 3.0

Input Set:

Output Set:

Started: 2009-03-24 15:42:52.907
Finished: 2009-03-24 15:42:55.625
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 718 ms
Total Warnings: 57
Total Errors: 0
No. of SeqIDs Defined: 69
Actual SeqID Count: 69

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)

Input Set:

Output Set:

Started: 2009-03-24 15:42:52.907
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Total Warnings: 57
Total Errors: 0
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Actual SeqID Count: 69

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
GILL, Gordon N.
YEO, Michele
LIN, Patrick S.
DAHMUS, Michael E.

<120> PHOSPHATASE REGULATION OF NUCLEIC ACID TRANSCRIPTION

<130> 00015-041US1

<140> 10552298

<141> 2006-06-12

<150> US 60/459,786

<151> 2003-04-01

<160> 69

<170> PatentIn version 3.5

<210> 1

<211> 783

<212> DNA

<213> Homo sapiens

<400> 1

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gtagctgacc tgctggacaa atggggggcc ttccggggcc ggctgtttcg agagtcctgc 540

gtcttccacc gggggaaacta cgtgaaggac ctgagccggt tgggtcgaga cctgcggcg 600

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gtggcctcgt ggttgacaa catgagtgac acagagctcc acgacctcct ccccttcttc 720

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tag

783

<210> 2
<211> 260
<212> PRT
<213> Homo sapiens

<400> 2

Met Asp Ser Ser Ala Val Ile Thr Gln Ile Ser Lys Glu Glu Ala Arg
1 5 10 15

Gly Pro Leu Arg Gly Lys Gly Asp Gln Lys Ser Ala Ala Ser Gln Lys
20 25 30

Pro Arg Ser Arg Gly Ile Leu His Ser Leu Phe Cys Cys Val Cys Arg
35 40 45

Asp Asp Gly Glu Ala Leu Pro Ala His Ser Gly Ala Pro Leu Leu Val
50 55 60

Glu Glu Asn Gly Ala Ile Pro Lys Thr Pro Val Gln Tyr Leu Leu Pro
65 70 75 80

Glu Ala Lys Ala Gln Asp Ser Asp Lys Ile Cys Val Val Ile Asp Leu
85 90 95

Asp Glu Thr Leu Val His Ser Ser Phe Lys Pro Val Asn Asn Ala Asp
100 105 110

Phe Ile Ile Pro Val Glu Ile Asp Gly Val Val His Gln Val Tyr Val
115 120 125

Leu Lys Arg Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Glu Leu
130 135 140

Phe Glu Cys Val Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp Pro
145 150 155 160

Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg Ala Arg Leu Phe
165 170 175

Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val Lys Asp Leu Ser
180 185 190

Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu Asp Asn Ser Pro

195

200

205

Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Pro Val Ala Ser Trp
210 215 220

Phe Asp Asn Met Ser Asp Thr Glu Leu His Asp Leu Leu Pro Phe Phe
225 230 235 240

Glu Gln Leu Ser Arg Val Asp Asp Val Tyr Ser Val Leu Arg Gln Pro
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Arg Pro Gly Ser
260

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<212> DNA
<213> Homo sapiens

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gcttcttaca tattccaccc cgagaatgca gtgcctgtgc agtccctggtt tgatgacatg 720
gcagacactg agttgctgaa cctgatccca atcttgagg agctgagcgg agcagaggac 780
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<210> 4

<211> 283
<212> PRT
<213> Homo sapiens

<400> 4

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Arg Gly Arg Asn Ile Phe Lys Ala Leu Phe Cys Cys Phe Arg Ala Gln
35 40 45

His Val Gly Gln Ser Ser Ser Ser Thr Glu Leu Ala Ala Tyr Lys Glu
50 55 60

Glu Ala Asn Thr Ile Ala Lys Ser Asp Leu Leu Gln Cys Leu Gln Tyr
65 70 75 80

Gln Phe Tyr Gln Ile Pro Gly Thr Cys Leu Leu Pro Glu Val Thr Glu
85 90 95

Glu Asp Gln Gly Arg Ile Cys Val Val Ile Asp Leu Asp Glu Thr Leu
100 105 110

Val His Ser Ser Phe Lys Pro Ile Asn Asn Ala Asp Phe Ile Val Pro
115 120 125

Ile Glu Ile Glu Gly Thr Thr His Gln Val Tyr Val Leu Lys Arg Pro
130 135 140

Tyr Val Asp Glu Phe Leu Arg Arg Met Gly Glu Leu Phe Glu Cys Val
145 150 155 160

Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp Pro Val Thr Asp Leu
165 170 175

Leu Asp Arg Cys Gly Val Phe Arg Ala Arg Leu Phe Arg Glu Ser Cys
180 185 190

Val Phe His Gln Gly Cys Tyr Val Lys Asp Leu Ser Arg Leu Gly Arg
195 200 205

Asp Leu Arg Lys Thr Leu Ile Leu Asp Asn Ser Pro Ala Ser Tyr Ile
210 215 220

Phe His Pro Glu Asn Ala Val Pro Val Gln Ser Trp Phe Asp Asp Met
225 230 235 240

Ala Asp Thr Glu Leu Leu Asn Leu Ile Pro Ile Phe Glu Glu Leu Ser
245 250 255

Gly Ala Glu Asp Val Tyr Thr Ser Leu Gly Ala Ala Ala Gly Pro Leu
260 265 270

Ala Cys Pro Ala Ser Lys Arg Arg Pro Ser Gln
275 280

<210> 5
<211> 798
<212> DNA
<213> Homo sapiens

<400> 5
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agcagcccca gtgtgcttcc gccactggtg gaggagaatg gtgggcttca gaagccacca 240
gctaagtacc ttcttccaga ggtgacggtg cttgactatg gaaagaaaatg tgtggtcatt 300
gatttagatg aaacatttgt gcacagttcg ttaaggcta ttagtaatgc tgattttatt 360
gttccggttg aaatcgatgg aactatacat caggtgtatg tgctgaagcg gccacatgtg 420
gacgagttcc tccagaggat gggcagctt tttgaatgtg tgctctttac tgccagcttg 480
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ggcgccggagc tgagcaaagt gatcattgtt gacaattccc ctgcctcata catttccat 660
cctgagaatg cagtgcctgt gcagtcctgg ttcgatgaca tgacggacac ggagctgctg 720
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agactctgca ataggttag 798

<210> 6

<211> 265
<212> PRT
<213> Homo sapiens

<400> 6

Met Asp Gly Pro Ala Ile Ile Thr Gln Val Thr Asn Pro Lys Glu Asp
1 5 10 15

Glu Gly Arg Leu Pro Gly Ala Gly Glu Lys Ala Ser Gln Cys Asn Val
20 25 30

Ser Leu Lys Lys Gln Arg Ser Arg Ser Ile Leu Ser Ser Phe Phe Cys
35 40 45

Cys Phe Arg Asp Tyr Asn Val Glu Ala Pro Pro Pro Ser Ser Pro Ser
50 55 60

Val Leu Pro Pro Leu Val Glu Glu Asn Gly Gly Leu Gln Lys Pro Pro
65 70 75 80

Ala Lys Tyr Leu Leu Pro Glu Val Thr Val Leu Asp Tyr Gly Lys Lys
85 90 95

Cys Val Val Ile Asp Leu Asp Glu Thr Leu Val His Ser Ser Phe Lys
100 105 110

Pro Ile Ser Asn Ala Asp Phe Ile Val Pro Val Glu Ile Asp Gly Thr
115 120 125

Ile His Gln Val Tyr Val Leu Lys Arg Pro His Val Asp Glu Phe Leu
130 135 140

Gln Arg Met Gly Gln Leu Phe Glu Cys Val Leu Phe Thr Ala Ser Leu
145 150 155 160

Ala Lys Tyr Ala Asp Pro Val Ala Asp Leu Leu Asp Arg Trp Gly Val
165 170 175

Phe Arg Ala Arg Leu Phe Arg Glu Ser Cys Val Phe His Arg Gly Asn
180 185 190

Tyr Val Lys Asp Leu Ser Arg Leu Gly Arg Glu Leu Ser Lys Val Ile
195 200 205

Ile Val Asp Asn Ser Pro Ala Ser Tyr Ile Phe His Pro Glu Asn Ala
210 215 220

Val Pro Val Gln Ser Trp Phe Asp Asp Met Thr Asp Thr Glu Leu Leu
225 230 235 240

Asp Leu Ile Pro Phe Phe Glu Gly Leu Ser Arg Glu Asp Asp Val Tyr
245 250 255

Ser Met Leu His Arg Leu Cys Asn Arg
260 265

<210> 7

<211> 642

<212> DNA

<213> Homo sapiens

<400> 7

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gacaagatct gcgtggcat cgacctggac gagaccctgg tgcacagctc cttcaagcca 180

gtgaacaacg cggacttcat catccctgtg gagattgatg gggtggtcca ccaggtctac 240

gtgttgaagc gtcctcacgt ggatgagttc ctgcagcgaa tggcgagct ctttgaatgt 300

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<210> 8

<211> 213

<212> PRT

<213> Homo sapiens

<400> 8

Met Met Gly Arg Pro Cys Leu Leu Thr Ala Gly Arg Pro Cys Leu Trp
1 5 10 15

Arg Arg Met Ala Pro Ser Leu Arg Gln Thr Pro Val Gln Tyr Leu Leu
20 25 30

Pro Glu Ala Lys Ala Gln Asp Ser Asp Lys Ile Cys Val Val Ile Asp
35 40 45

Leu Asp Glu Thr Leu Val His Ser Ser Phe Lys Pro Val Asn Asn Ala
50 55 60

Asp Phe Ile Ile Pro Val Glu Ile Asp Gly Val Val His Gln Val Tyr
65 70 75 80

Val Leu Lys Arg Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Glu
85 90 95

Leu Phe Glu Cys Val Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp
100 105 110

Pro Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg Ala Arg Leu
115 120 125

Phe Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val Lys Asp Leu
130 135 140

Ser Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu Asp Asn Ser
145 150 155 160

Pro Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Pro Val Ala Ser
165 170 175

Trp Phe Asp Asn Met Ser Asp Thr Glu Leu His Asp Leu Leu Pro Phe
180 185 190

Phe Glu Gln Leu Ser Arg Val Asp Asp Val Tyr Ser Val Leu Arg Gln
195 200 205

Pro Arg Pro Gly Ser
210

<210> 9
<211> 783
<212> DNA
<213> Drosophila

<400> 9
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ccccctgcttg tggaggagaa tggcgccatc cctaagaccc cagtccaata cctgctccct 240

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gtgcacagct cttcaagcc agtgaacaac gcggacttca tcatccctgt ggagattgtat 360

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atgggcgagc tcttgaatg tgtgctgttc actgctagcc tcgccaagta cgcagaccca 480

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tag 783

<210> 10
<211> 260
<212> PRT
<213> Drosophila

<400> 10

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Gly Pro Leu Arg Gly Lys Gly Asp Gln Lys Ser Ala Ala Ser Gln Lys
20 25 30

Pro Arg Ser Arg Gly Ile Leu His Ser Leu Phe Cys Cys Val Cys Arg
35 40 45

Asp Asp Gly Glu Ala Leu Pro Ala His Ser Gly Ala Pro Leu Leu Val
50 55 60

Glu Glu Asn Gly Ala Ile Pro Lys Thr Pro Val Gln Tyr Leu Leu Pro
65 70 75 80

Glu Ala Lys Ala Gln Asp Ser Asp Lys Ile Cys Val Val Ile Glu Leu
85 90 95

Asn Glu Thr Leu Val His Ser Ser Phe Lys Pro Val Asn Asn Ala Asp
100 105 110

Phe Ile Ile Pro Val Glu Ile Asp Gly Val Val His Gln Val Tyr Val
115 120 125

Leu Lys Arg Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Glu Leu
130 135 140

Phe Glu Cys Val Leu Phe Thr Ala Ser Leu Ala Lys Tyr Ala Asp Pro
145 150 155 160

Val Ala Asp Leu Leu Asp Lys Trp Gly Ala Phe Arg Ala Arg Leu Phe
165 170 175

Arg Glu Ser Cys Val Phe His Arg Gly Asn Tyr Val Lys Asp Leu Ser
180 185 190

Arg Leu Gly Arg Asp Leu Arg Arg Val Leu Ile Leu Asp Asn Ser Pro
195 200 205

Ala Ser Tyr Val Phe His Pro Asp Asn Ala Val Pro Val Ala Ser Trp
210 215 220

Phe Asp Asn Met Ser Asp Thr Glu Leu His Asp Leu Leu Pro Phe Phe
225 230 235 240

Glu Gln Leu Ser Arg Val Asp Asp Val Tyr Ser Val Leu Arg Gln Pro
245 250 255

Arg Pro Gly Ser
260

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<211> 642
<212> DNA
<213> Drosophila

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gacaagatct gcgtggtcat cgarctgaac gagaccctgg tgcacagctc cttcaagcca 180
gtgaacaacg cggacttcat catccctgtg gagattgatg gggtggtcca ccaggtctac 240
gtgttgaagc gtctcacgt ggatgagttc ctgcagcgaa tggcgagct ctttgaatgt 300
tgctgttca ctgcttagcct cgccaagtac gcagacccag tag